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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2007; month=12; day=10; hr=14; min=12; sec=3; ms=680; ]

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## Validated By CRFValidator v 1.0.3

Application No: 10716293 Version No: 3.0

Input Set:

Output Set:

**Started:** 2007-11-19 16:59:18.503

Finished: 2007-11-19 16:59:22.389

**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 886 ms

Total Warnings: 220

Total Errors: 0

No. of SeqIDs Defined: 220

Actual SeqID Count: 220

Error code		Error Description									
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W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(19)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(20)

Input Set:

Output Set:

**Started:** 2007-11-19 16:59:18.503

Finished: 2007-11-19 16:59:22.389

**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 886 ms

Total Warnings: 220

Total Errors: 0

No. of SeqIDs Defined: 220

Actual SeqID Count: 220

Error code Error Description

This error has occured more than 20 times, will not be displayed

## SEQUENCE LISTING

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5

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<110> MASSIA, STEPHEN P.
      EHTESHAMI, GHOLAM R.
<120> THERAPEUTIC BIOCONJUGATES
<130> AZTE:015US
<140> 10716293
<141> 2003-11-17
<150> 10/295,734
<151> 2002-11-15
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caa tat
Gln Tyr
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10

15

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aat ttc cta gag aag ttt gtt cag ggt ctc gat atc ggc cct acc aaa
                                                                      48
Asn Phe Leu Glu Lys Phe Val Gln Gly Leu Asp Ile Gly Pro Thr Lys
                                    10
acc cag gtc ggt ctg ata caa tat gcg aat aat cca cgc tgg ttc aat
                                                                      96
Thr Gln Val Gly Leu Ile Gln Tyr Ala Asn Asn Pro Arg Trp Phe Asn
cta aat act tat aag act aag gaa gag atg att gtt gct acc tcc cag
                                                                     144
Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln
       35
                            40
                                                45
act agc cag tac ggc ggt gat cta aca aat aca ttc gga gcg atc cag
                                                                     192
Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile Gln
    50
                        55
tat gcg cga aaa tat gcg tat tca gcg gcc tct gga ggc cgt cga agt
                                                                     240
Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg Ser
                    70
                                        75
                                                            80
                                                                     261
gca aca ctt aaa gta atg gtg
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             5
                                   10
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           20
                           25
Leu Asn Thr Tyr Lys Thr Lys Glu Glu Met Ile Val Ala Thr Ser Gln
      35
                         40
Thr Ser Gln Tyr Gly Gly Asp Leu Thr Asn Thr Phe Gly Ala Ile Gln
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Tyr Ala Arg Lys Tyr Ala Tyr Ser Ala Ala Ser Gly Gly Arg Arg Ser
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Ala Thr Leu Lys Val Met Val
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tac aac gtc gac aca gaa tct gca ctt tta tat cag ggc ccg cat aat
                                                                    48
Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn
                                   10
                                                                    96
aca ctg ttt ggc tac agt tgg ctc cac tcc cat gga gct cat aga tgg
Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp
          20
cta ctg gta gga gcg cca aca gca atg tgg tta gca atg gca agc gtt
                                                                   144
Leu Leu Val Gly Ala Pro Thr Ala Met Trp Leu Ala Met Ala Ser Val
                           40
```

att aat cct ggg gcc atc tat aga tgc aga ata gga aaa aac cca ggg

192

Ile Asn Pro Gly Ala Ile Tyr Arg Cys Arg Ile Gly Lys Asn Pro Gly 55 cag acg tgt gaa ttg caa ttg ggt tca ttc cac ggt gag ccc ggc ggt 240 Gln Thr Cys Glu Leu Gln Leu Gly Ser Phe His Gly Glu Pro Gly Gly 70 75 288 aag act tgt cta gag gaa aga gat cac caa tgg ctt ggg gtg acc ctc Lys Thr Cys Leu Glu Glu Arg Asp His Gln Trp Leu Gly Val Thr Leu 85 294 tcg aga Ser Arg <210> 10 <211> 98 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Integrin <400> 10 Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn 10 15 1 5 Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp 20 25 Leu Leu Val Gly Ala Pro Thr Ala Met Trp Leu Ala Met Ala Ser Val 35 40 45 Ile Asn Pro Gly Ala Ile Tyr Arg Cys Arg Ile Gly Lys Asn Pro Gly 50 55 Gln Thr Cys Glu Leu Gln Leu Gly Ser Phe His Gly Glu Pro Gly Gly 65 70 75 8.0 Lys Thr Cys Leu Glu Glu Arg Asp His Gln Trp Leu Gly Val Thr Leu 90 85 Ser Arg

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cag gat tat gta aag aaa ttc ggc gaa cat ttt gca agt tgt caa gca
                                                                     48
Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala
ggg ata tcc tcg ttc tat acg aaa gac tta atc gta atg ggt gca cca
                                                                     96
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro
           20
                               25
gga tct tca tac tgg aca gga agc tta ttt gta tac atg att acc act
                                                                    144
Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr
        35
                           40
                                               45
                                                                    156
aat aag tat aaa
Asn Lys Tyr Lys
   50
<210> 12
<211> 52
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Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala
                                  10
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro
                            25
                                                  30
          20
Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr
       35
                         40
Asn Lys Tyr Lys
   50
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<212> DNA

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                                                                     48
Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala
ggg ata tcc tcg ttc tat acg aaa gac tta atc gta atg ggt gca cca
                                                                     96
Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro
           20
                               25
gga tct tca tac tgg aca gga agc tta ttt gta tac atg att acc act
                                                                    144
Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr
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                           40
aat aag tat aaa
                                                                    156
Asn Lys Tyr Lys
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Gln Asp Tyr Val Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala
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Gly Ile Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro
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                                                  30
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Gly Ser Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Met Ile Thr Thr
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Asn Lys Tyr Lys
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Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys Asn Glu Asn Lys Leu
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cca aca gga gga
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Pro Thr Gly Gly
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Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys Asn Glu Asn Lys Leu
               5
                                   10
Pro Thr Gly Gly
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gga gga gca cca cag cat gaa caa ata gga aaa
                                                                      33
Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys
               5
                                    10
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Ser Tyr Trp Thr Gly Ser
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Ser Tyr Trp Thr Gly Ser
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atg gga gca cca gga agt agt tat tgg aca gga
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Met Gly Ala Pro Gly Ser Ser Tyr Trp Thr Gly
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Met Gly Ala Pro Gly Ser Ser Tyr Trp Thr Gly
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                                                                     48
Tyr Asn Val Asp Thr Glu Ser Ala Leu Leu Tyr Gln Gly Pro His Asn
aca ttg ttt ggg tat agt tgg ctt cat agt cat gga gca cac aga tgg
                                                                      96
Thr Leu Phe Gly Tyr Ser Trp Leu His Ser His Gly Ala His Arg Trp
            20
                                25
                                                    30
                                                                     111
ctg cta gta ggc gca
Leu Leu Val Gly Ala
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<221> CDS

<220>

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<u> </u>	v	0/		Ċ

Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile Lys His 1 5 10 15

Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro Asp Leu 20 25 30

Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Gly Tyr Gln Asp Tyr Val 35 40 45

Lys Lys Phe Gly Glu His Phe Ala Ser Cys Gln Ala Gly Ile Ser Ser 50 55 60

Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala 65 70 75

<210> 27 <211> 222

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Integrin

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<222> (1)..(222)

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tac atg att acc act aac aag tat aaa gcg ttt tta ggg aag caa aat 48
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1 5 10 15

cag gtg aag cca gga agt tat tta ggg tat agt gta ggt gcc ggc cat 96
Gln Val Lys Pro Gly Ser Tyr Leu Gly Tyr Ser Val Gly Ala Gly His
20 25 30

ttc aga ag